

# SEQUENCE LISTING

<110> Mahajan, Muktar A  
Samuels, Herbert H

<120> NIF-1 IS A NOVEL CO-TRANSDUCER THAT INTERACTS WITH AND  
REGULATES THE ACTIVITY OF THE NUCLEAR HORMONE RECEPTOR  
CO-ACTIVATOR, NRC

<130> 57953/1151

<140>

<141>

<150> 60/405,752

<151> 2002-08-23

<160> 14

<170> PatentIn Ver. 2.1

<210> 1

<211> 4439

<212> DNA

<213> Human

<400> 1

```

gacctcgtcg atgccggagt cagagaggaa cgtggctacg aaagcctcgg agtgaagttc 60
ccagacccta cgccccgctg tcaggcagcc cgccgatcag atggaggaga acgaggtgga 120
gagcagcagc gacgcggccc ctgggcctgg ccggcccgag gagccctctg agagcggcct 180
gggtgtgggc acctcagaag ccgtgtccgc cgacagcagc gacgccgcgg ccgccccggg 240
gcaggcagag gccgatgact ctggcgtggg gcaaagctcg gaccgcggca gccgttctca 300
ggaggaggtg tctgagagca gctcgagcgc agacccccctg cctaatagct acctccctga 360
ttcatcgtct gtgtctcatg ggccagtggc aggggtgaca ggcgggtccc cagcacttgt 420
gcaactctagt gcactccag acctccaacat gctggtgtcc gactgcacag ctctctctc 480
ggacctgggc tcggccatcg acaagatcat cgagtccacc atcggggccg acctcatcca 540
gaactgcata actgtgacca gtgctgagga tggcggggcc gagaccacac ggtacctgat 600
cctacagggc ccagatgatg gagcccccat gacatcacca atgtccagtt ccaccttggc 660
ccacagccta gcagccattg aggccctggc agatggcccc acatccacat ccacatgcct 720
ggaggcacag ggtgggcccc gctccccggg gcagctgccc ccagcctccg gtgccgaaga 780
gccggacctg cagagcctgg aggccatgat ggaggtggtg gtggtgcagc agttcaaagt 840
caagatgtgc cagtaccgga gcagaccaa ggccacactg ctgcgccaca tgcgggaacg 900
ccacttccgt ccagtagcag cagccgcagc agcagctggt aaaaaaggac gtctacggaa 960
gtggagcacc tccaccaaga gccaagagga agaggagga gaggaggagg acgatgatga 1020
cattgtagac gctggagcca ttgatgacct ggaggaggat agcgactata atccagctga 1080
ggatgagccc cgaggccggc agcttcggct ccagcgcgcc acccccagta cccaagggcc 1140
ccgaaggaga cctggccggc cccggaagct gccccgcctg gagatctcag acctcccaga 1200
tggtgtggaa ggagagcctc tagtgagttc ccagagtgga cagagccctc cagagccaca 1260

```

ggatccccgag gctccccagct cctcaggcccc aggacacctg gtggccatgg gcaaggtgag 1320  
 caggaccccc gtggaagctg gtgtgagcca gtcagatgca gagaacgcag cccctcctg 1380  
 cccggatgag catgacactc tgccccggcg ccgagggtcga ccttccaggc gcttcctagg 1440  
 caagaaatac cgcaagtact attacaagtc gcccaaacca cttttgaggc ccttcctgtg 1500  
 ccgcatctgt ggttctcgtt ttctgtccca cgaggacctg cgcttccacg tcaactccca 1560  
 tgaggctggc gatccccagc tcttcaagtg cctgcagtgc agctatcgtt cccgccgctg 1620  
 gtccctcgtc aaggagcaca tgttcaacca cgtgggcagc aagccctaca agtgtgacga 1680  
 gtgcagctac accagtgtct accggaagga cgtcattcgg cacgccgctg tgcacagccg 1740  
 ggaccggaag aagaggccag atccgactcc aaagctgagc tctttccctt gccctgtgtg 1800  
 tggccgtgtg taccatctgc agaaaagact cacgcagcac atgaagacgc acagcactga 1860  
 gaagccccac atgtgtgaca agtgtggaag gtcccttaag aagcgctaca ccttcaaaat 1920  
 gcacctgctc acgcacatcc aggtgtgtgc caaccgcagg ttcaagtgtg agttctgtga 1980  
 gtttggttgt gaagacaaga aggcactgct gaaccaccag ttgtccacg tcagtgcaca 2040  
 gcccttcaaa tgcagctttt gtccctaccg caccttccga gaggacttct tgctgtccca 2100  
 tgtggctgtc aagcacacag gggccaagcc ctctgcctgt gactactgcc acttcagcac 2160  
 acggcacaaag aagaacctgc gcctgcacgt acgggtgccg cacgcaagca gcttcgagga 2220  
 atgggggagc cgccaccctg aggagccccc ctcccgccgt cgcctcttct tctctctgca 2280  
 gcagattgag gagctgaagc agcagcacag tggggccctt ggaccacctc ccagttcccc 2340  
 aggacctcct gagatacccc cagaggcgac aactttccag tcatctgagg ctccctcatt 2400  
 gctctgttct gacacctggt gcggcgccac catcatctac cagcaaggag ctgaggagtc 2460  
 gacagcgatg gccacgcaga cagccttgga tcttctgctg aacatgagtg ctacgcggga 2520  
 actggggggc acagccctgc aggtggctgt ggtgaagtcg gaagatgtgg aagcagggtt 2580  
 agcatccctt ggtgggcagc cctcccttga aggtgccact ccacagggtg tcaccctcca 2640  
 cgtggcagag ccagggggcg gtgcagcagc cgagagccag ctaggccctc ctgacctacc 2700  
 gcagatcacc ctggcacctg gtccatttgg tgggactggc tacagtgtca tcacagcacc 2760  
 ccctatggag gaggaacat cagctcctgg cacaccttac agcgaggagc ccgcaggaga 2820  
 ggcagcccag gctgtggttg tgagtgcac cctaaaagaa gctggcacc actacatcat 2880  
 ggctactgat ggtaccagt tgcaccacat tgagctcacc gcagatggct ccatctcctt 2940  
 cccaagtcca gatgctctgg cctctggtgc caaatggccc ctgctgcagt gtgggggact 3000  
 gccagagac ggccctgagc ccccatctcc agccaagacc cactgcgtag gggactccca 3060  
 gagctctgcc tctcacctc ctgcaaccag caaagccctg ggccctggcag tgcccccgctc 3120  
 accgccatct gcagccactg ctgcatcaaa gaagttttcc tgcaagatct gtgccgaggc 3180  
 cttccctggc cgagctgaga tggagagtca caagcgggccc cacgctgggc ctggtgcctt 3240  
 caagtgcctc gactgcctct tcagtgcctg ccagtggccc gaggtccggg cgcacatggc 3300  
 acagcactca agcctacggc cccaccagtg tagccagtgc agctttgcct ccaagaacaa 3360  
 gaaggacctg cgtcggcaca tgctgactca cacaagagg aagccttttg catgccacct 3420  
 ctgcgggcag cgtttcaacc gtaacgggca cctcaagttc cacatccagc ggctgcacag 3480  
 tctgatggg aggaagtcag gaacccttac agcccgggccc cctaccaga cccaaccca 3540  
 gaccatcatc ctgaacagt atgacgaaac actggccacc ctgcacactg cactccagtc 3600  
 cagtcacggg gtccctgggc cagagcggct acagcaggca ctgagccagg aacacatcat 3660  
 cgttgcccag gaacagacag tgaccaatca ggaggaagcc gcctacatcc aagagatcac 3720  
 cacggcagat ggccagaccg tacagcacct ggtgacctcc gacaaccagg tgcagtatat 3780  
 catctcccag gatggtgtcc agcacctgct cccccaggaa tatgttgttg tccctgaagg 3840  
 ccatcacatc caggtacagg agggccagat cacacacatc cagtatgaac aaggagcccc 3900  
 gttccttcag gactcccaga tccagtatgt gcctgtgtcc ccaggccagc agcttgtcac 3960  
 acaggctcaa cttgaggctg cagcacactc agctgtcaca gcagtggctg atgctgccat 4020  
 ggcccaagcc cagggcctgt ttggtacaga cgagacagtg cccgaacaca ttcaacagct 4080  
 gcagcaccag ggcctcagat acgacgtcat caccctggcc gatgactgag ccccgagggc 4140

ccaacacaga tcatggattt gcggccagct ctctggtggg tagggggcca ccaggactca 4200  
cctccctctt catttaggat ctccagatac tggatagcca gcacccctctc attcccaggg 4260  
agccagacct gtgctgttgg ggtaggggc agccatgggc ccagccagg acatgctggg 4320  
tgccccagcc tgcaggcagg ctttgggaga gaaatttatt tttgtttggg tggaccact 4380  
ggcctgtcag tctcaataaa gggaccggag tccagtctg aacagcttaa aaaaaaaaa 4439

<210> 2

<211> 1357

<212> PRT

<213> Human

<400> 2

Ser Ser Gln Thr Leu Arg Pro Ala Val Arg Gln Pro Ala Asp Gln Met  
1 5 10 15

Glu Glu Asn Glu Val Glu Ser Ser Ser Asp Ala Ala Pro Gly Pro Gly  
20 25 30

Arg Pro Glu Glu Pro Ser Glu Ser Gly Leu Gly Val Gly Thr Ser Glu  
35 40 45

Ala Val Ser Ala Asp Ser Ser Asp Ala Ala Ala Ala Pro Gly Gln Ala  
50 55 60

Glu Ala Asp Asp Ser Gly Val Gly Gln Ser Ser Asp Arg Gly Ser Arg  
65 70 75 80

Ser Gln Glu Glu Val Ser Glu Ser Ser Ser Ser Ala Asp Pro Leu Pro  
85 90 95

Asn Ser Tyr Leu Pro Asp Ser Ser Ser Val Ser His Gly Pro Val Ala  
100 105 110

Gly Val Thr Gly Gly Pro Pro Ala Leu Val His Ser Ser Ala Leu Pro  
115 120 125

Asp Pro Asn Met Leu Val Ser Asp Cys Thr Ala Ser Ser Ser Asp Leu  
130 135 140

Gly Ser Ala Ile Asp Lys Ile Ile Glu Ser Thr Ile Gly Pro Asp Leu  
145 150 155 160

Ile Gln Asn Cys Ile Thr Val Thr Ser Ala Glu Asp Gly Gly Ala Glu  
165 170 175

Thr Thr Arg Tyr Leu Ile Leu Gln Gly Pro Asp Asp Gly Ala Pro Met  
180 185 190

Thr Ser Pro Met Ser Ser Ser Thr Leu Ala His Ser Leu Ala Ala Ile  
 195 200 205  
 Glu Ala Leu Ala Asp Gly Pro Thr Ser Thr Ser Thr Cys Leu Glu Ala  
 210 215 220  
 Gln Gly Gly Pro Ser Ser Pro Val Gln Leu Pro Pro Ala Ser Gly Ala  
 225 230 235 240  
 Glu Glu Pro Asp Leu Gln Ser Leu Glu Ala Met Met Glu Val Val Val  
 245 250 255  
 Val Gln Gln Phe Lys Cys Lys Met Cys Gln Tyr Arg Ser Ser Thr Lys  
 260 265 270  
 Ala Thr Leu Leu Arg His Met Arg Glu Arg His Phe Arg Pro Val Ala  
 275 280 285  
 Ala Ala Ala Ala Ala Ala Gly Lys Lys Gly Arg Leu Arg Lys Trp Ser  
 290 295 300  
 Thr Ser Thr Lys Ser Gln Glu Glu Glu Gly Pro Glu Glu Glu Asp Asp  
 305 310 315 320  
 Asp Asp Ile Val Asp Ala Gly Ala Ile Asp Asp Leu Glu Glu Asp Ser  
 325 330 335  
 Asp Tyr Asn Pro Ala Glu Asp Glu Pro Arg Gly Arg Gln Leu Arg Leu  
 340 345 350  
 Gln Arg Pro Thr Pro Ser Thr Pro Arg Pro Arg Arg Arg Pro Gly Arg  
 355 360 365  
 Pro Arg Lys Leu Pro Arg Leu Glu Ile Ser Asp Leu Pro Asp Gly Val  
 370 375 380  
 Glu Gly Glu Pro Leu Val Ser Ser Gln Ser Gly Gln Ser Pro Pro Glu  
 385 390 395 400  
 Pro Gln Asp Pro Glu Ala Pro Ser Ser Ser Gly Pro Gly His Leu Val  
 405 410 415  
 Ala Met Gly Lys Val Ser Arg Thr Pro Val Glu Ala Gly Val Ser Gln  
 420 425 430  
 Ser Asp Ala Glu Asn Ala Ala Pro Ser Cys Pro Asp Glu His Asp Thr  
 435 440 445

Leu Pro Arg Arg Arg Gly Arg Pro Ser Arg Arg Phe Leu Gly Lys Lys  
 450 455 460

Tyr Arg Lys Tyr Tyr Tyr Lys Ser Pro Lys Pro Leu Leu Arg Pro Phe  
 465 470 475 480

Leu Cys Arg Ile Cys Gly Ser Arg Phe Leu Ser His Glu Asp Leu Arg  
 485 490 495

Phe His Val Asn Ser His Glu Ala Gly Asp Pro Gln Leu Phe Lys Cys  
 500 505 510

Leu Gln Cys Ser Tyr Arg Ser Arg Arg Trp Ser Ser Leu Lys Glu His  
 515 520 525

Met Phe Asn His Val Gly Ser Lys Pro Tyr Lys Cys Asp Glu Cys Ser  
 530 535 540

Tyr Thr Ser Val Tyr Arg Lys Asp Val Ile Arg His Ala Ala Val His  
 545 550 555 560

Ser Arg Asp Arg Lys Lys Arg Pro Asp Pro Thr Pro Lys Leu Ser Ser  
 565 570 575

Phe Pro Cys Pro Val Cys Gly Arg Val Tyr Pro Met Gln Lys Arg Leu  
 580 585 590

Thr Gln His Met Lys Thr His Ser Thr Glu Lys Pro His Met Cys Asp  
 595 600 605

Lys Cys Gly Lys Ser Phe Lys Lys Arg Tyr Thr Phe Lys Met His Leu  
 610 615 620

Leu Thr His Ile Gln Ala Val Ala Asn Arg Arg Phe Lys Cys Glu Phe  
 625 630 635 640

Cys Glu Phe Val Cys Glu Asp Lys Lys Ala Leu Leu Asn His Gln Leu  
 645 650 655

Ser His Val Ser Asp Lys Pro Phe Lys Cys Ser Phe Cys Pro Tyr Arg  
 660 665 670

Thr Phe Arg Glu Asp Phe Leu Leu Ser His Val Ala Val Lys His Thr  
 675 680 685

Gly Ala Lys Pro Phe Ala Cys Glu Tyr Cys His Phe Ser Thr Arg His  
 690 695 700

Lys Lys Asn Leu Arg Leu His Val Arg Cys Arg His Ala Ser Ser Phe  
 705 710 715 720  
 Glu Glu Trp Gly Arg Arg His Pro Glu Glu Pro Pro Ser Arg Arg Arg  
 725 730 735  
 Pro Phe Phe Ser Leu Gln Gln Ile Glu Glu Leu Lys Gln Gln His Ser  
 740 745 750  
 Ala Ala Pro Gly Pro Pro Pro Ser Ser Pro Gly Pro Pro Glu Ile Pro  
 755 760 765  
 Pro Glu Ala Thr Thr Phe Gln Ser Ser Glu Ala Pro Ser Leu Leu Cys  
 770 775 780  
 Ser Asp Thr Leu Gly Gly Ala Thr Ile Ile Tyr Gln Gln Gly Ala Glu  
 785 790 795 800  
 Glu Ser Thr Ala Met Ala Thr Gln Thr Ala Leu Asp Leu Leu Leu Asn  
 805 810 815  
 Met Ser Ala Gln Arg Glu Leu Gly Gly Thr Ala Leu Gln Val Ala Val  
 820 825 830  
 Val Lys Ser Glu Asp Val Glu Ala Gly Leu Ala Ser Pro Gly Gly Gln  
 835 840 845  
 Pro Ser Pro Glu Gly Ala Thr Pro Gln Val Val Thr Leu His Val Ala  
 850 855 860  
 Glu Pro Gly Gly Gly Ala Ala Ala Glu Ser Gln Leu Gly Pro Pro Asp  
 865 870 875 880  
 Leu Pro Gln Ile Thr Leu Ala Pro Gly Pro Phe Gly Gly Thr Gly Tyr  
 885 890 895  
 Ser Val Ile Thr Ala Pro Pro Met Glu Glu Gly Thr Ser Ala Pro Gly  
 900 905 910  
 Thr Pro Tyr Ser Glu Glu Pro Ala Gly Glu Ala Ala Gln Ala Val Val  
 915 920 925  
 Val Ser Asp Thr Leu Lys Glu Ala Gly Thr His Tyr Ile Met Ala Thr  
 930 935 940  
 Asp Gly Thr Gln Leu His His Ile Glu Leu Thr Ala Asp Gly Ser Ile  
 945 950 955 960

Ser Phe Pro Ser Pro Asp Ala Leu Ala Ser Gly Ala Lys Trp Pro Leu  
 965 970 975  
 Leu Gln Cys Gly Gly Leu Pro Arg Asp Gly Pro Glu Pro Pro Ser Pro  
 980 985 990  
 Ala Lys Thr His Cys Val Gly Asp Ser Gln Ser Ser Ala Ser Ser Pro  
 995 1000 1005  
 Pro Ala Thr Ser Lys Ala Leu Gly Leu Ala Val Pro Pro Ser Pro Pro  
 1010 1015 1020  
 Ser Ala Ala Thr Ala Ala Ser Lys Lys Phe Ser Cys Lys Ile Cys Ala  
 1025 1030 1035 1040  
 Glu Ala Phe Pro Gly Arg Ala Glu Met Glu Ser His Lys Arg Ala His  
 1045 1050 1055  
 Ala Gly Pro Gly Ala Phe Lys Cys Pro Asp Cys Pro Phe Ser Ala Arg  
 1060 1065 1070  
 Gln Trp Pro Glu Val Arg Ala His Met Ala Gln His Ser Ser Leu Arg  
 1075 1080 1085  
 Pro His Gln Cys Ser Gln Cys Ser Phe Ala Ser Lys Asn Lys Lys Asp  
 1090 1095 1100  
 Leu Arg Arg His Met Leu Thr His Thr Lys Glu Lys Pro Phe Ala Cys  
 1105 1110 1115 1120  
 His Leu Cys Gly Gln Arg Phe Asn Arg Asn Gly His Leu Lys Phe His  
 1125 1130 1135  
 Ile Gln Arg Leu His Ser Pro Asp Gly Arg Lys Ser Gly Thr Pro Thr  
 1140 1145 1150  
 Ala Arg Ala Pro Thr Gln Thr Pro Thr Gln Thr Ile Ile Leu Asn Ser  
 1155 1160 1165  
 Asp Asp Glu Thr Leu Ala Thr Leu His Thr Ala Leu Gln Ser Ser His  
 1170 1175 1180  
 Gly Val Leu Gly Pro Glu Arg Leu Gln Gln Ala Leu Ser Gln Glu His  
 1185 1190 1195 1200  
 Ile Ile Val Ala Gln Glu Gln Thr Val Thr Asn Gln Glu Glu Ala Ala  
 1205 1210 1215

Tyr Ile Gln Glu Ile Thr Thr Ala Asp Gly Gln Thr Val Gln His Leu  
1220 1225 1230

Val Thr Ser Asp Asn Gln Val Gln Tyr Ile Ile Ser Gln Asp Gly Val  
1235 1240 1245

Gln His Leu Leu Pro Gln Glu Tyr Val Val Val Pro Glu Gly His His  
1250 1255 1260

Ile Gln Val Gln Glu Gly Gln Ile Thr His Ile Gln Tyr Glu Gln Gly  
1265 1270 1275 1280

Ala Pro Phe Leu Gln Glu Ser Gln Ile Gln Tyr Val Pro Val Ser Pro  
1285 1290 1295

Gly Gln Gln Leu Val Thr Gln Ala Gln Leu Glu Ala Ala Ala His Ser  
1300 1305 1310

Ala Val Thr Ala Val Ala Asp Ala Ala Met Ala Gln Ala Gln Gly Leu  
1315 1320 1325

Phe Gly Thr Asp Glu Thr Val Pro Glu His Ile Gln Gln Leu Gln His  
1330 1335 1340

Gln Gly Ile Glu Tyr Asp Val Ile Thr Leu Ala Asp Asp  
1345 1350 1355

<210> 3  
<211> 1342  
<212> PRT  
<213> Human

<400> 3  
Met Glu Glu Asn Glu Val Glu Ser Ser Ser Asp Ala Ala Pro Gly Pro  
1 5 10 15

Gly Arg Pro Glu Glu Pro Ser Glu Ser Gly Leu Gly Val Gly Thr Ser  
20 25 30

Glu Ala Val Ser Ala Asp Ser Ser Asp Ala Ala Ala Ala Pro Gly Gln  
35 40 45

Ala Glu Ala Asp Asp Ser Gly Val Gly Gln Ser Ser Asp Arg Gly Ser  
50 55 60

Arg Ser Gln Glu Glu Val Ser Glu Ser Ser Ser Ser Ala Asp Pro Leu



65		70		75		80									
Pro	Asn	Ser	Tyr	Leu	Pro	Asp	Ser	Ser	Ser	Val	Ser	His	Gly	Pro	Val
				85					90					95	
Ala	Gly	Val	Thr	Gly	Gly	Pro	Pro	Ala	Leu	Val	His	Ser	Ser	Ala	Leu
			100					105					110		
Pro	Asp	Pro	Asn	Met	Leu	Val	Ser	Asp	Cys	Thr	Ala	Ser	Ser	Ser	Asp
		115					120					125			
Leu	Gly	Ser	Ala	Ile	Asp	Lys	Ile	Ile	Glu	Ser	Thr	Ile	Gly	Pro	Asp
	130					135					140				
Leu	Ile	Gln	Asn	Cys	Ile	Thr	Val	Thr	Ser	Ala	Glu	Asp	Gly	Gly	Ala
145					150					155					160
Glu	Thr	Thr	Arg	Tyr	Leu	Ile	Leu	Gln	Gly	Pro	Asp	Asp	Gly	Ala	Pro
			165					170						175	
Met	Thr	Ser	Pro	Met	Ser	Ser	Ser	Thr	Leu	Ala	His	Ser	Leu	Ala	Ala
			180					185					190		
Ile	Glu	Ala	Leu	Ala	Asp	Gly	Pro	Thr	Ser	Thr	Ser	Thr	Cys	Leu	Glu
	195						200					205			
Ala	Gln	Gly	Gly	Pro	Ser	Ser	Pro	Val	Gln	Leu	Pro	Pro	Ala	Ser	Gly
	210					215					220				
Ala	Glu	Glu	Pro	Asp	Leu	Gln	Ser	Leu	Glu	Ala	Met	Met	Glu	Val	Val
225					230					235					240
Val	Val	Gln	Gln	Phe	Lys	Cys	Lys	Met	Cys	Gln	Tyr	Arg	Ser	Ser	Thr
			245						250					255	
Lys	Ala	Thr	Leu	Leu	Arg	His	Met	Arg	Glu	Arg	His	Phe	Arg	Pro	Val
			260					265					270		
Ala	Ala	Ala	Ala	Ala	Ala	Ala	Gly	Lys	Lys	Gly	Arg	Leu	Arg	Lys	Trp
	275						280					285			
Ser	Thr	Ser	Thr	Lys	Ser	Gln	Glu	Glu	Glu	Gly	Pro	Glu	Glu	Glu	Asp
	290					295					300				
Asp	Asp	Asp	Ile	Val	Asp	Ala	Gly	Ala	Ile	Asp	Asp	Leu	Glu	Glu	Asp
305					310					315					320
Ser	Asp	Tyr	Asn	Pro	Ala	Glu	Asp	Glu	Pro	Arg	Gly	Arg	Gln	Leu	Arg

	325		330		335										
Leu	Gln	Arg	Pro	Thr	Pro	Ser	Thr	Pro	Arg	Pro	Arg	Arg	Arg	Pro	Gly
			340					345					350		
Arg	Pro	Arg	Lys	Leu	Pro	Arg	Leu	Glu	Ile	Ser	Asp	Leu	Pro	Asp	Gly
			355				360					365			
Val	Glu	Gly	Glu	Pro	Leu	Val	Ser	Ser	Gln	Ser	Gly	Gln	Ser	Pro	Pro
			370				375				380				
Glu	Pro	Gln	Asp	Pro	Glu	Ala	Pro	Ser	Ser	Ser	Gly	Pro	Gly	His	Leu
385					390					395					400
Val	Ala	Met	Gly	Lys	Val	Ser	Arg	Thr	Pro	Val	Glu	Ala	Gly	Val	Ser
				405					410					415	
Gln	Ser	Asp	Ala	Glu	Asn	Ala	Ala	Pro	Ser	Cys	Pro	Asp	Glu	His	Asp
			420					425					430		
Thr	Leu	Pro	Arg	Arg	Arg	Gly	Arg	Pro	Ser	Arg	Arg	Phe	Leu	Gly	Lys
			435				440					445			
Lys	Tyr	Arg	Lys	Tyr	Tyr	Tyr	Lys	Ser	Pro	Lys	Pro	Leu	Leu	Arg	Pro
	450					455					460				
Phe	Leu	Cys	Arg	Ile	Cys	Gly	Ser	Arg	Phe	Leu	Ser	His	Glu	Asp	Leu
465					470					475					480
Arg	Phe	His	Val	Asn	Ser	His	Glu	Ala	Gly	Asp	Pro	Gln	Leu	Phe	Lys
				485					490					495	
Cys	Leu	Gln	Cys	Ser	Tyr	Arg	Ser	Arg	Arg	Trp	Ser	Ser	Leu	Lys	Glu
			500					505					510		
His	Met	Phe	Asn	His	Val	Gly	Ser	Lys	Pro	Tyr	Lys	Cys	Asp	Glu	Cys
			515				520					525			
Ser	Tyr	Thr	Ser	Val	Tyr	Arg	Lys	Asp	Val	Ile	Arg	His	Ala	Ala	Val
	530					535				540					
His	Ser	Arg	Asp	Arg	Lys	Lys	Arg	Pro	Asp	Pro	Thr	Pro	Lys	Leu	Ser
545					550				555					560	
Ser	Phe	Pro	Cys	Pro	Val	Cys	Gly	Arg	Val	Tyr	Pro	Met	Gln	Lys	Arg
				565				570					575		
Leu	Thr	Gln	His	Met	Lys	Thr	His	Ser	Thr	Glu	Lys	Pro	His	Met	Cys

580	585	590
Asp Lys Cys Gly Lys Ser Phe Lys Lys Arg Tyr Thr Phe Lys Met His		
595	600	605
Leu Leu Thr His Ile Gln Ala Val Ala Asn Arg Arg Phe Lys Cys Glu		
610	615	620
Phe Cys Glu Phe Val Cys Glu Asp Lys Lys Ala Leu Leu Asn His Gln		
625	630	635
Leu Ser His Val Ser Asp Lys Pro Phe Lys Cys Ser Phe Cys Pro Tyr		
	645	650
Arg Thr Phe Arg Glu Asp Phe Leu Leu Ser His Val Ala Val Lys His		
	660	665
Thr Gly Ala Lys Pro Phe Ala Cys Glu Tyr Cys His Phe Ser Thr Arg		
	675	680
His Lys Lys Asn Leu Arg Leu His Val Arg Cys Arg His Ala Ser Ser		
	690	695
Phe Glu Glu Trp Gly Arg Arg His Pro Glu Glu Pro Pro Ser Arg Arg		
705	710	715
Arg Pro Phe Phe Ser Leu Gln Gln Ile Glu Glu Leu Lys Gln Gln His		
	725	730
Ser Ala Ala Pro Gly Pro Pro Pro Ser Ser Pro Gly Pro Pro Glu Ile		
	740	745
Pro Pro Glu Ala Thr Thr Phe Gln Ser Ser Glu Ala Pro Ser Leu Leu		
	755	760
Cys Ser Asp Thr Leu Gly Gly Ala Thr Ile Ile Tyr Gln Gln Gly Ala		
	770	775
Glu Glu Ser Thr Ala Met Ala Thr Gln Thr Ala Leu Asp Leu Leu Leu		
785	790	795
Asn Met Ser Ala Gln Arg Glu Leu Gly Gly Thr Ala Leu Gln Val Ala		
	805	810
Val Val Lys Ser Glu Asp Val Glu Ala Gly Leu Ala Ser Pro Gly Gly		
	820	825
Gln Pro Ser Pro Glu Gly Ala Thr Pro Gln Val Val Thr Leu His Val		
		830

835		840		845
Ala Glu Pro Gly Gly Gly	Ala Ala Ala Glu Ser	Gln Leu Gly Pro Pro		
850	855	860		
Asp Leu Pro Gln Ile Thr	Leu Ala Pro Gly Pro Phe	Gly Gly Thr Gly		
865	870	875	880	
Tyr Ser Val Ile Thr	Ala Pro Pro Met Glu Glu	Gly Thr Ser Ala Pro		
	885	890	895	
Gly Thr Pro Tyr Ser	Glu Glu Pro Ala Gly Glu	Ala Ala Gln Ala Val		
	900	905	910	
Val Val Ser Asp Thr	Leu Lys Glu Ala Gly Thr	His Tyr Ile Met Ala		
	915	920	925	
Thr Asp Gly Thr Gln	Leu His His Ile Glu Leu	Thr Ala Asp Gly Ser		
	930	935	940	
Ile Ser Phe Pro Ser	Pro Asp Ala Leu Ala Ser	Gly Ala Lys Trp Pro		
945	950	955	960	
Leu Leu Gln Cys Gly	Gly Leu Pro Arg Asp Gly	Pro Glu Pro Pro Ser		
	965	970	975	
Pro Ala Lys Thr His	Cys Val Gly Asp Ser Gln	Ser Ser Ala Ser Ser		
	980	985	990	
Pro Pro Ala Thr Ser	Lys Ala Leu Gly Leu Ala	Val Pro Pro Ser Pro		
	995	1000	1005	
Pro Ser Ala Ala Thr	Ala Ala Ser Lys Lys Phe	Ser Cys Lys Ile Cys		
1010	1015	1020		
Ala Glu Ala Phe Pro	Gly Arg Ala Glu Met Glu	Ser His Lys Arg Ala		
1025	1030	1035	1040	
His Ala Gly Pro Gly	Ala Phe Lys Cys Pro Asp	Cys Pro Phe Ser Ala		
	1045	1050	1055	
Arg Gln Trp Pro Glu	Val Arg Ala His Met Ala	Gln His Ser Ser Leu		
	1060	1065	1070	
Arg Pro His Gln Cys	Ser Gln Cys Ser Phe Ala	Ser Lys Asn Lys Lys		
	1075	1080	1085	
Asp Leu Arg Arg His	Met Leu Thr His Thr	Lys Glu Lys Pro Phe	Ala	

1090	1095	1100
Cys His Leu Cys Gly Gln Arg Phe Asn Arg Asn Gly His Leu Lys Phe		
1105	1110	1115 1120
His Ile Gln Arg Leu His Ser Pro Asp Gly Arg Lys Ser Gly Thr Pro		
	1125	1130 1135
Thr Ala Arg Ala Pro Thr Gln Thr Pro Thr Gln Thr Ile Ile Leu Asn		
	1140	1145 1150
Ser Asp Asp Glu Thr Leu Ala Thr Leu His Thr Ala Leu Gln Ser Ser		
	1155	1160 1165
His Gly Val Leu Gly Pro Glu Arg Leu Gln Gln Ala Leu Ser Gln Glu		
	1170	1175 1180
His Ile Ile Val Ala Gln Glu Gln Thr Val Thr Asn Gln Glu Glu Ala		
1185	1190	1195 1200
Ala Tyr Ile Gln Glu Ile Thr Thr Ala Asp Gly Gln Thr Val Gln His		
	1205	1210 1215
Leu Val Thr Ser Asp Asn Gln Val Gln Tyr Ile Ile Ser Gln Asp Gly		
	1220	1225 1230
Val Gln His Leu Leu Pro Gln Glu Tyr Val Val Val Pro Glu Gly His		
	1235	1240 1245
His Ile Gln Val Gln Glu Gly Gln Ile Thr His Ile Gln Tyr Glu Gln		
	1250	1255 1260
Gly Ala Pro Phe Leu Gln Glu Ser Gln Ile Gln Tyr Val Pro Val Ser		
1265	1270	1275 1280
Pro Gly Gln Gln Leu Val Thr Gln Ala Gln Leu Glu Ala Ala Ala His		
	1285	1290 1295
Ser Ala Val Thr Ala Val Ala Asp Ala Ala Met Ala Gln Ala Gln Gly		
	1300	1305 1310
Leu Phe Gly Thr Asp Glu Thr Val Pro Glu His Ile Gln Gln Leu Gln		
	1315	1320 1325
His Gln Gly Ile Glu Tyr Asp Val Ile Thr Leu Ala Asp Asp		
1330	1335	1340

<210> 4  
 <211> 4339  
 <212> DNA  
 <213> Human

<400> 4  
 atggaggaga acgaggtgga gagcagcagc gacgcggccc ctgggcctgg ccggccccgag 60  
 gagccctctg agagcggcct ggggtgtggc acctcagaag ccgtgtccgc cgacagcagc 120  
 gacgccgcgg ccgccccggg gcaggcagag gccgatgact ctggcgtggg gcaaagctcg 180  
 gaccgcggca gccgttctca ggaggaggta tctgagagca gctcgagcgc agacccccctg 240  
 cctaatagct acctccctga ttcctcgtct gtgtctcatg ggccagtggc aggggtgaca 300  
 ggcgttcccc cagcacttgt gcactctagt gcactcccag accccaacat gctggtgtcc 360  
 gactgcacag ctctctctc ggacctgggc tcggccatcg acaagatcat cgagtccacc 420  
 atcgggcccc acctcatcca gaactgcata actgtgacca gtgctgagga tggcggggcc 480  
 gagaccacac ggtacctgat cctacagggc ccagatgatg gagcccccat gacatcacca 540  
 atgtccagtt ccaccttggc ccacagccta gcagccattg aggccctggc agatggcccc 600  
 acatccacat ccacatgcct ggaggcacag ggtgggcccc gctccccggg gcagctgccc 660  
 ccagcctccg gtgccgaaga gccggacctg cagagcctgg aggccatgat ggaggtggtg 720  
 gtggtgcagc agttcaaag caagatgtgc cagtaccgga gcagcaccaa ggccacactg 780  
 ctgcgccaca tgcgggaacg ccacttccgt ccagtagcag cagccgcagc agcagctggt 840  
 aaaaaaggac gtctacgga gtggagcacc tccaccaaga gccaagagga agagggacca 900  
 gaggaggagg acgatgatga cattgtagac gctggagcca ttgatgacct ggaggaggat 960  
 agcgactata atccagctga ggatgagccc cgaggccggc agcttcggct ccagcgcccc 1020  
 acccccagta cccaaggcc ccgaaggaga cctggccggc cccggaagct gccccgcctg 1080  
 gagatctcag acctcccaga tgggtgtgga ggagagcctc tagtgagttc ccagagtgga 1140  
 cagagccctc cagagccaca ggatcccgag gctcccagct cctcaggccc aggacacctg 1200  
 gtggccatgg gcaaggtgag caggaccctt gtggaagctg gtgtgagcca gtcagatgca 1260  
 gagaacgcag cccctcctg cccggatgag catgacactc tgccccggcg ccgaggtcga 1320  
 ccttcaggc gcttcctagg caagaaatac cgcaagtact attacaagtc gcccaaacca 1380  
 cttttgaggc ctttcctgtg ccgcctctgt ggttctcgct ttctgtcca cgaggacctg 1440  
 cgcttcacg tcaactccca tgaggctggc gatccccagc tcttcaagtg cctgcagtgc 1500  
 agctatcggt cccgccgctg gtcctcgctc aaggagcaca tgttcaacca cgtgggcagc 1560  
 aagccctaca agtgtgacga gtgcagctac accagtgtct accggaagga cgtcattcgg 1620  
 cagcgcgtg tgcacagccg ggaccggaag aagaggccag atccgactcc aaagctgagc 1680  
 tctttccct gccctgtgtg tggccgtgtg taccctatgc agaaaagact cacgcagcac 1740  
 atgaagacgc acagcactga gaagccccac atgtgtgaca agtgtggaaa gtcctttaag 1800  
 aagcgctaca ctttcaaat gcacctgtc acgcacatcc aggctgttg caaccgcagg 1860  
 ttcaagtgtg agttctgtga gtttgtttgt gaagacaaga aggcactgct gaaccaccag 1920  
 ttgtccacg tcagtgacaa gcccttcaaa tgcagctttt gtccctaccg caccttccga 1980  
 gaggacttct tgctgtccca tgtggctgtc aagcacacag gggccaagcc cttcgccctgt 2040  
 gagtactgcc acttcagcac acggcacaag aagaacctgc gcctgcacgt acggtgccga 2100  
 cacgcaagca gcttcgagga atgggggagg cgccaccctg aggagcccc ctcgcccgct 2160  
 cgcctcttct tctctctgca gcagattgag gagctgaagc agcagcacag tgcggcccct 2220  
 ggaccacctc ccagttcccc aggacctcct gagatacccc cagaggcgac aactttccag 2280  
 tcctctgagg ctccctcatt gctctgttct gacacctgg gcggcgccac catcatctac 2340  
 cagcaaggag ctgaggagtc gacagcgatg gccacgcaga cagccttga tcttctgctg 2400  
 aacatgagtg ctacgcggga actggggggc acagccctgc aggtggctgt ggtgaagtcg 2460  
 gaagatgtgg aagcagggtt agcatcccct ggtgggcagc cctcccctga aggtgccact 2520

ccacaggtgg	tcacccctcca	cgtggcagag	ccagggggcg	gtgcagcagc	cgagagccag	2580
ctaggccctc	ctgacctacc	gcagatcacc	ctggcacctg	gtccatttgg	tgggactggc	2640
tacagtgtca	tcacagcacc	ccctatggag	gagggaacat	cagctcctgg	cacaccttac	2700
agcgaggagc	ccgcaggaga	ggcagcccag	gctgtggttg	tgagtgcacac	cctaaaagaa	2760
gctggcacc	actacatcat	ggctactgat	ggtacccagt	tgcaccacat	tgagctcacc	2820
gcagatggct	ccatctcctt	cccaagtcca	gatgctctgg	cctctggtgc	caaattggccc	2880
ctgctgcagt	gtgggggact	gcccagagac	ggccctgagc	ccccatctcc	agccaagacc	2940
cactgcgtag	gggactccca	gagctctgcc	tcctcacctc	ctgcaaccag	caaagccctg	3000
ggcctggcag	tgcccccgtc	accgccatct	gcagccactg	ctgcatcaaa	gaagttttcc	3060
tgcaagatct	gtgccgaggc	cttccttggc	cgagctgaga	tggagagtca	caagcggggc	3120
cacgtggggc	ctggtgcctt	caagtgcctc	gactgcccct	tcagtgcctg	ccagtggccc	3180
gaggtccggg	cgcacatggc	acagcactca	agcctacggc	cccaccagtg	tagccagtgc	3240
agctttgcct	ccaagaacaa	gaaggacctg	cgtcggcaca	tgctgactca	cacaaaggag	3300
aagccttttg	catgccacct	ctgcgggcag	cgtttcaacc	gtaacgggca	cctcaagtcc	3360
cacatccagc	ggctgcacag	tcctgatggg	aggaagtcag	gaacccctac	agcccggggc	3420
cctacccaga	ccccaaccca	gacctcatc	ctgaacagtg	atgacgaaac	actggccacc	3480
ctgcacactg	cactccagtc	cagtcacggg	gtcctggggc	cagagcggct	acagcaggca	3540
ctgagccagg	aacacatcat	cgttgcccag	gaacagacag	tgaccaatca	ggaggaagcc	3600
gcctacatcc	aagagatcac	cacggcagat	ggccagaccg	tacagcacct	ggtgacctcc	3660
gacaaccagg	tgcagtatat	catctcccag	gatggtgtcc	agcacctgct	cccccaggaa	3720
tatgttgtgg	tcctgaagg	ccatcacatc	caggtacagg	agggccagat	cacacacatc	3780
cagtatgaac	aaggagcccc	gttccttcag	gagtcccaga	tccagtatgt	gcctgtgtcc	3840
ccaggccagc	agcttgtcac	acaggctcaa	cttgaggctg	cagcacactc	agctgtcaca	3900
gcagtggctg	atgctgccat	ggcccaagcc	cagggcctgt	ttggtacaga	cgagacagtg	3960
cccgaacaca	ttcaacagct	gcagcaccag	ggcatcgagt	acgacgtcat	caccctggcc	4020
gatgactgag	ccccgagggc	ccaacacaga	tcatggattt	gcggccagct	ctcctggggg	4080
tagggggcca	ccaggactca	cctccctctt	catttaggat	ctccagatac	tggatagcca	4140
gcacctctc	attcccaggg	agccagacct	gtgctgttgg	ggttaggggc	agccatgggc	4200
cccagccagg	acatgctggg	tgccccagcc	tgcaggcagg	ctttgggaga	gaaatttatt	4260
tttgtttggg	tggacccact	ggcctgtcag	tctcaataaa	gggaccggag	tccagtcctg	4320
aacagcttaa	aaaaaaaaa					4339

<210> 5

<211> 2662

<212> DNA

<213> Human

<400> 5

atggaggaga	acgaggtgga	gagcagcagc	gacgcggccc	ctgggcctgg	ccggccccgag	60
gagccctctg	agagcggcct	gggtgtgggc	acctcagaag	ccgtgtccgc	cgacagcagc	120
gacgcgcggg	ccgccccggg	gcaggcagag	gccgatgact	ctggcgtggg	gcaaagctcg	180
gaccgcggca	gccgttctca	ggaggaggta	tctgagagca	gctcgagcgc	agacccctcg	240
cctaatagct	acctccctga	ttcatcgtct	gtgtctcatg	ggccagtggc	aggggtgaca	300
ggcggctccc	cagcacttgt	gcactctagt	gcactcccag	acccaacat	gctggtgtcc	360
gactgcacag	cttcctcctc	ggacctgggc	tcggccatcg	acaagatcat	cgagtccacc	420
atcggggccg	acctcatcca	gaactgcata	actgtgacca	gtgctgagga	tggcggggcc	480
gagaccacac	ggtacctgat	cctacagggc	ccagatgatg	gagcccccat	gacatcacca	540

```

atgtccagtt cccccagttc cccaggacct cctgagatac cccagagggc gacaactttc 600
cagtcacatctg aggtccctc attgctctgt tctgacaccc tgggcggcgc caccatcatc 660
taccagcaag gagctgagga gtcgacagcg atggccacgc agacagcctt ggatcttctg 720
ctgaacatga gtgctcagcg ggaactgggg ggcacagccc tgcaggtggc tgtggtgaag 780
tcggaagatg tggaagcagg gttagcatcc cctggtgggc agccctcccc tgaaggtgcc 840
actccacagg tggtcaccct ccacgtggca gagccagggg gcggtgcagc agccgagagc 900
cagctaggcc ctctgacct accgcagatc accctggcac ctggtccatt tgggtgggact 960
ggctacagtg tcatcacagc accccctatg gaggagggaa catcagctcc tggcacacct 1020
tacagcgagg agcccgagg agaggcagcc caggctgtgg ttgtgagtga caccctaaaa 1080
gaagctggca cccactacat catggctact gatggtaccc agttgcacca cattgagctc 1140
accgcagatg gctccatctc cttcccaagt ccagatgctc tggcctctgg tgccaaatgg 1200
cccctgctgc agtgtggggg actgccaga gacggccctg agcccccatc tccagccaag 1260
accactgcg taggggactc ccagagctct gcctcctcac ctctgcaac cagcaaagcc 1320
ctgggcctgg cagtgtcccc gtcaccgcca tctgcagcca ctgctgcac aaagaagttt 1380
tcctgcaaga tctgtgccga ggccttcctt ggccgagctg agatggagag tcacaagcgg 1440
gccacgctg ggctggtgc cttcaagtgc cccgactgcc ccttcagtgc ccgccagtgg 1500
cccagggtcc gggcgccatc ggcacagcac tcaagcctac ggccccacca gtgtagccag 1560
tgcagctttg cctccaagaa caagaaggac ctgcgtcggc acatgctgac tcacacaaag 1620
gagaagcctt ttgcatgcc cctctgcggg cagcgtttca accgtaacgg gcacctcaag 1680
ttccacatcc agcggctgca cagtccatgat gggaggaagt caggaaacccc tacagcccg 1740
gcccctaccc agaccccaac ccagaccatc atcctgaaca gtgatgacga aacactggcc 1800
accctgcaca ctgcaactca gtccagtcac ggggtcctgg gccagagcg gctacagcag 1860
gactgagcc aggaacacat catcgttgcc caggaaacaga cagtgaccaa tcaggaggaa 1920
gccgcctaca tccaagagat caccacggca gatggccaga ccgtacagca cctggtgacc 1980
tccgacaacc aggtgcagta tatcatctcc caggatggtg tccagcacct gctccccag 2040
gaatatgttg tggtcctga aggccatcac atccaggtac aggagggcca gatcacacac 2100
atccagtatg aacaaggagc cccgttcctt caggagtccc agatccagta tgtgcctgtg 2160
tccccaggcc agcagcttgt cacacaggct caacttgagg ctgcagcaca ctgagctgtc 2220
acagcagtgg ctgatgctgc catggcccaa gccaggggc tgtttggtac agacgagaca 2280
gtgcccgaac acattcaaca gctgcagcac cagggcacgc agtacgacgt catcacctg 2340
gccgatgact gagccccgag ggcccaaac agatcatgga tttgcggcca gctctcctgg 2400
gggtaggggg ccaccaggac tcacctccct cttcathtag gatctccaga tactggatag 2460
ccagcatcct ctcatccca gggagccaga cctgtgctgt tgggggttagg ggcagccatg 2520
ggccccagcc aggacatgct ggggtgcccc gctgcaggc aggccttggg agagaaattt 2580
atTTTTgttt ggggtggacc actggcctgt cagtctcaat aaagggaccg gagtccagtc 2640
ctgaacagct taaaaaaaaa aa 2662

```

<210> 6

<211> 783

<212> PRT

<213> Human

<400> 6

Met Glu Glu Asn Glu Val Glu Ser Ser Ser Asp Ala Ala Pro Gly Pro

1

5

10

15

Gly Arg Pro Glu Glu Pro Ser Glu Ser Gly Leu Gly Val Gly Thr Ser



20					25					30						
Glu	Ala	Val	Ser	Ala	Asp	Ser	Ser	Asp	Ala	Ala	Ala	Ala	Ala	Pro	Gly	Gln
35					40					45						
Ala	Glu	Ala	Asp	Asp	Ser	Gly	Val	Gly	Gln	Ser	Ser	Asp	Arg	Gly	Ser	
50					55					60						
Arg	Ser	Gln	Glu	Glu	Val	Ser	Glu	Ser	Ser	Ser	Ser	Ala	Asp	Pro	Leu	
65					70					75					80	
Pro	Asn	Ser	Tyr	Leu	Pro	Asp	Ser	Ser	Ser	Val	Ser	His	Gly	Pro	Val	
85					90					95						
Ala	Gly	Val	Thr	Gly	Gly	Pro	Pro	Ala	Leu	Val	His	Ser	Ser	Ala	Leu	
100					105					110						
Pro	Asp	Pro	Asn	Met	Leu	Val	Ser	Asp	Cys	Thr	Ala	Ser	Ser	Ser	Asp	
115					120					125						
Leu	Gly	Ser	Ala	Ile	Asp	Lys	Ile	Ile	Glu	Ser	Thr	Ile	Gly	Pro	Asp	
130					135					140						
Leu	Ile	Gln	Asn	Cys	Ile	Thr	Val	Thr	Ser	Ala	Glu	Asp	Gly	Gly	Ala	
145					150					155					160	
Glu	Thr	Thr	Arg	Tyr	Leu	Ile	Leu	Gln	Gly	Pro	Asp	Asp	Gly	Ala	Pro	
165					170					175						
Met	Thr	Ser	Pro	Met	Ser	Ser	Ser	Pro	Ser	Ser	Pro	Gly	Pro	Pro	Glu	
180					185					190						
Ile	Pro	Pro	Glu	Ala	Thr	Thr	Phe	Gln	Ser	Ser	Glu	Ala	Pro	Ser	Leu	
195					200					205						
Leu	Cys	Ser	Asp	Thr	Leu	Gly	Gly	Ala	Thr	Ile	Ile	Tyr	Gln	Gln	Gly	
210					215					220						
Ala	Glu	Glu	Ser	Thr	Ala	Met	Ala	Thr	Gln	Thr	Ala	Leu	Asp	Leu	Leu	
225					230					235					240	
Leu	Asn	Met	Ser	Ala	Gln	Arg	Glu	Leu	Gly	Gly	Thr	Ala	Leu	Gln	Val	
245					250					255						
Ala	Val	Val	Lys	Ser	Glu	Asp	Val	Glu	Ala	Gly	Leu	Ala	Ser	Pro	Gly	
260					265					270						
Gly	Gln	Pro	Ser	Pro	Glu	Gly	Ala	Thr	Pro	Gln	Val	Val	Thr	Leu	His	

275		280		285
Val Ala Glu Pro Gly Gly Gly Ala Ala Ala Glu Ser Gln Leu Gly Pro				
290		295		300
Pro Asp Leu Pro Gln Ile Thr Leu Ala Pro Gly Pro Phe Gly Gly Thr				
305		310		315
				320
Gly Tyr Ser Val Ile Thr Ala Pro Pro Met Glu Glu Gly Thr Ser Ala				
		325		330
				335
Pro Gly Thr Pro Tyr Ser Glu Glu Pro Ala Gly Glu Ala Ala Gln Ala				
		340		345
				350
Val Val Val Ser Asp Thr Leu Lys Glu Ala Gly Thr His Tyr Ile Met				
		355		360
				365
Ala Thr Asp Gly Thr Gln Leu His His Ile Glu Leu Thr Ala Asp Gly				
		370		375
				380
Ser Ile Ser Phe Pro Ser Pro Asp Ala Leu Ala Ser Gly Ala Lys Trp				
385		390		395
				400
Pro Leu Leu Gln Cys Gly Gly Leu Pro Arg Asp Gly Pro Glu Pro Pro				
		405		410
				415
Ser Pro Ala Lys Thr His Cys Val Gly Asp Ser Gln Ser Ser Ala Ser				
		420		425
				430
Ser Pro Pro Ala Thr Ser Lys Ala Leu Gly Leu Ala Val Pro Pro Ser				
		435		440
				445
Pro Pro Ser Ala Ala Thr Ala Ala Ser Lys Lys Phe Ser Cys Lys Ile				
		450		455
				460
Cys Ala Glu Ala Phe Pro Gly Arg Ala Glu Met Glu Ser His Lys Arg				
465		470		475
				480
Ala His Ala Gly Pro Gly Ala Phe Lys Cys Pro Asp Cys Pro Phe Ser				
		485		490
				495
Ala Arg Gln Trp Pro Glu Val Arg Ala His Met Ala Gln His Ser Ser				
		500		505
				510
Leu Arg Pro His Gln Cys Ser Gln Cys Ser Phe Ala Ser Lys Asn Lys				
		515		520
				525
Lys Asp Leu Arg Arg His Met Leu Thr His Thr Lys Glu Lys Pro Phe				

530	535	540
Ala Cys His Leu Cys Gly Gln Arg Phe Asn Arg Asn Gly His Leu Lys 545	550	555 560
Phe His Ile Gln Arg Leu His Ser Pro Asp Gly Arg Lys Ser Gly Thr 565	570	575
Pro Thr Ala Arg Ala Pro Thr Gln Thr Pro Thr Gln Thr Ile Ile Leu 580	585	590
Asn Ser Asp Asp Glu Thr Leu Ala Thr Leu His Thr Ala Leu Gln Ser 595	600	605
Ser His Gly Val Leu Gly Pro Glu Arg Leu Gln Gln Ala Leu Ser Gln 610	615	620
Glu His Ile Ile Val Ala Gln Glu Gln Thr Val Thr Asn Gln Glu Glu 625	630	635 640
Ala Ala Tyr Ile Gln Glu Ile Thr Thr Ala Asp Gly Gln Thr Val Gln 645	650	655
His Leu Val Thr Ser Asp Asn Gln Val Gln Tyr Ile Ile Ser Gln Asp 660	665	670
Gly Val Gln His Leu Leu Pro Gln Glu Tyr Val Val Val Pro Glu Gly 675	680	685
His His Ile Gln Val Gln Glu Gly Gln Ile Thr His Ile Gln Tyr Glu 690	695	700
Gln Gly Ala Pro Phe Leu Gln Glu Ser Gln Ile Gln Tyr Val Pro Val 705	710	715 720
Ser Pro Gly Gln Gln Leu Val Thr Gln Ala Gln Leu Glu Ala Ala Ala 725	730	735
His Ser Ala Val Thr Ala Val Ala Asp Ala Ala Met Ala Gln Ala Gln 740	745	750
Gly Leu Phe Gly Thr Asp Glu Thr Val Pro Glu His Ile Gln Gln Leu 755	760	765
Gln His Gln Gly Ile Glu Tyr Asp Val Ile Thr Leu Ala Asp Asp 770	775	780

<210> 7  
 <211> 2778  
 <212> DNA  
 <213> Rat

<400> 7  
 atgttcaacc acgtgggcag caaacctac aagtgtgacg aatgcagcta caccagtgtc 60  
 taccgcaagg atgttattcg gcatgcggcc gtgcacagcc aggaccgaaa gaagaggccg 120  
 gatccgaccc caaagctgag ctctttccct tgcccagtggt gtggccgtgt ataccccatg 180  
 cagaagagac taacacagca catgaagact cacagtacgg agaagccaca catgtgcgat 240  
 aagtgtggaa agtcctttaa gaagcggtag accttcaaaa tgcacttgct cacacacatc 300  
 caggctgttg ccaaccgcag attcaagtgt gagttctgcg agtttgtttg tgaggacaag 360  
 aaagcactgt tgaaccacca gctgtcccat gttagcgaca agcccttcaa atgcagcttt 420  
 tgtccctatc gcaccttccg tgaggacttc ctgctgtctc atgtggctgt gaagcacaca 480  
 ggagccaagc ccttcgctg tgagtactgc cacttcagca ctgcgccaca gaagaacctg 540  
 cgcctgcatg tacggtgccg acatgcgaac agctttgagg agtgggggag gcgccacct 600  
 gaggagcctc catcccgtag ccgccccatc ttctctttgc aacagataga gaagctgaag 660  
 cagcagcaca gtgcggcccc tggccctccc ctgagttcag caggccccga ggccccccaa 720  
 gaaccagcac ctttcagtc acctgagact cccccactac tctgtcctga tgccctaggt 780  
 ggtgccacaa tcatctacca gcaaggcgct gaggagtcca ctgcaatggc cactcagaca 840  
 gccttggatc tactgttgaa catgagcgcc caacgagagc tggggggccac agccttgag 900  
 gtggctgtgg tgaagtcaga ggacgtggag gcagagttga catctactgc taggcagcct 960  
 tcctctgaag acaccactcc acgggtggtg acacttcatg tggcagagtc agggagcagt 1020  
 gtggcagctg agagccagct agggccgtct gacctacagc agattgcctt gccacctggg 1080  
 ccattcagtg gggccagcta cagtgtcatc acagcacccc ccgtggaggg gagggcatca 1140  
 gcttccggcc caccttacag ggaagaacct ccaggagagg cagcccaggc tgtggttg 1200  
 aacgacactc tcaaggaagc tggcacccac tatatcatgg cagctgatgg gaccagttg 1260  
 caccacattg agctgactgc agatggctcc atctccttcc caagcccaga tactctggcc 1320  
 cctggaacca agtggccctt gctgcagtgt ggaggggccac ctgagatagg tcctgaggtt 1380  
 ctgtctccaa cgaagaccca ccatacggga ggctcccagg gctcttccac cccacccctt 1440  
 gcaaccagcc atgccctagg cctgctagta cccactccc caccgtctgc agcagcttca 1500  
 tcaacaaaga agttctcctg caaggtgtgc tcagaggcct tccctagccg tgagagatg 1560  
 gagagtcaca agcgggcccc tgcctggcct gctgccttca agtgccctga ctgccccttc 1620  
 agtgctcgcc aatggcccga ggtccgggct cacatggcac agcactccag tctgaggccc 1680  
 caccagtga atcagtgtag ctctgcctcc aagaacaaga aggacctcag gcggcacatg 1740  
 ctgacacaca ccaatgagaa gcctttctca tgccacgtct gtgggcagcg tttcaacagg 1800  
 aacgggcacc tcaaattcca catccagcgg ctacatagca tcgatggtag aaagactggg 1860  
 acttctacag cccgagcccc agcccagacc atcatcctca atagtgaaga ggagacactg 1920  
 gccacactgc acactgcctt ccagtcgaat caggggactc tggggacaga gaggctacag 1980  
 caggcactga gccaggagca tatcattgtg gccagggaac agacagtggc caatcaggag 2040  
 gaagctacct acatccagga aatcacggca gatggccaga cggtagagca tctggtgacc 2100  
 tcagacaacc aggttcagta tatcatctct caggatggtg tccagcactt gctgcctcag 2160  
 gagtacgttg tggctccctga tggccatcac atccaggttc aggaggcca gatcacacac 2220  
 attcagtatg agcaaggcac cccattccta caggagtccc agatccagta tgtacctgta 2280  
 tccccagcc agcagcttgt caccagagct cagcttgaag ctgcagcaca ttctgctgtt 2340  
 acagtggctg atgctgcat ggcccaagcc cagggcctgt ttggcactga ggaggcagtg 2400  
 ccggaacaca ttcaacagct gcagcatcag ggcacagag acgacgtcat caccctctcg 2460  
 gatgactgag cctcaaaggc ccaacgctga tcgtggatat cggggccagc tctcctggag 2520

actagggact ttcctgtcct acttagggcc tccaganact ggacagttag tgtcccttga 2580  
 ctccaaagga gccagacctg tgctcttggg gggcagccaa gggctccagc caggacatgc 2640  
 tgggtgtgtc agcctgtctg caggctttgg gagagaaatt tatttttgtt ttgatggacc 2700  
 cactggctcc tgtctcaata aagggaccag agtccagctc ttgccaaaaa aaaaaaaaaa 2760  
 aaaaaaaaaa aaaaaaaaaa 2778

<210> 8  
 <211> 822  
 <212> PRT  
 <213> Rat

<400> 8  
 Met Phe Asn His Val Gly Ser Lys Pro Tyr Lys Cys Asp Glu Cys Ser  
 1 5 10 15  
 Tyr Thr Ser Val Tyr Arg Lys Asp Val Ile Arg His Ala Ala Val His  
 20 25 30  
 Ser Gln Asp Arg Lys Lys Arg Pro Asp Pro Thr Pro Lys Leu Ser Ser  
 35 40 45  
 Phe Pro Cys Pro Val Cys Gly Arg Val Tyr Pro Met Gln Lys Arg Leu  
 50 55 60  
 Thr Gln His Met Lys Thr His Ser Thr Glu Lys Pro His Met Cys Asp  
 65 70 75 80  
 Lys Cys Gly Lys Ser Phe Lys Lys Arg Tyr Thr Phe Lys Met His Leu  
 85 90 95  
 Leu Thr His Ile Gln Ala Val Ala Asn Arg Arg Phe Lys Cys Glu Phe  
 100 105 110  
 Cys Glu Phe Val Cys Glu Asp Lys Lys Ala Leu Leu Asn His Gln Leu  
 115 120 125  
 Ser His Val Ser Asp Lys Pro Phe Lys Cys Ser Phe Cys Pro Tyr Arg  
 130 135 140  
 Thr Phe Arg Glu Asp Phe Leu Leu Ser His Val Ala Val Lys His Thr  
 145 150 155 160  
 Gly Ala Lys Pro Phe Ala Cys Glu Tyr Cys His Phe Ser Thr Arg His  
 165 170 175  
 Lys Lys Asn Leu Arg Leu His Val Arg Cys Arg His Ala Asn Ser Phe  
 180 185 190

Glu Glu Trp Gly Arg Arg His Pro Glu Glu Pro Pro Ser Arg Arg Arg  
 195 200 205  
 Pro Ile Phe Ser Leu Gln Gln Ile Glu Lys Leu Lys Gln Gln His Ser  
 210 215 220  
 Ala Ala Pro Gly Pro Pro Leu Ser Ser Ala Gly Pro Glu Ala Pro Gln  
 225 230 235 240  
 Glu Pro Ala Pro Phe Gln Ser Pro Glu Thr Pro Pro Leu Leu Cys Pro  
 245 250 255  
 Asp Ala Leu Gly Gly Ala Thr Ile Ile Tyr Gln Gln Gly Ala Glu Glu  
 260 265 270  
 Ser Thr Ala Met Ala Thr Gln Thr Ala Leu Asp Leu Leu Leu Asn Met  
 275 280 285  
 Ser Ala Gln Arg Glu Leu Gly Ala Thr Ala Leu Gln Val Ala Val Val  
 290 295 300  
 Lys Ser Glu Asp Val Glu Ala Glu Leu Thr Ser Thr Ala Arg Gln Pro  
 305 310 315 320  
 Ser Ser Glu Asp Thr Thr Pro Arg Val Val Thr Leu His Val Ala Glu  
 325 330 335  
 Ser Gly Ser Ser Val Ala Ala Glu Ser Gln Leu Gly Pro Ser Asp Leu  
 340 345 350  
 Gln Gln Ile Ala Leu Pro Pro Gly Pro Phe Ser Gly Ala Ser Tyr Ser  
 355 360 365  
 Val Ile Thr Ala Pro Pro Val Glu Gly Arg Ala Ser Ala Ser Gly Pro  
 370 375 380  
 Pro Tyr Arg Glu Glu Pro Pro Gly Glu Ala Ala Gln Ala Val Val Val  
 385 390 395 400  
 Asn Asp Thr Leu Lys Glu Ala Gly Thr His Tyr Ile Met Ala Ala Asp  
 405 410 415  
 Gly Thr Gln Leu His His Ile Glu Leu Thr Ala Asp Gly Ser Ile Ser  
 420 425 430  
 Phe Pro Ser Pro Asp Thr Leu Ala Pro Gly Thr Lys Trp Pro Leu Leu  
 435 440 445

Gln Cys Gly Gly Pro Pro Arg Asp Gly Pro Glu Val Leu Ser Pro Thr  
 450 455 460

Lys Thr His His Thr Gly Gly Ser Gln Gly Ser Ser Thr Pro Pro Pro  
 465 470 475 480

Ala Thr Ser His Ala Leu Gly Leu Leu Val Pro His Ser Pro Pro Ser  
 485 490 495

Ala Ala Ala Ser Ser Thr Lys Lys Phe Ser Cys Lys Val Cys Ser Glu  
 500 505 510

Ala Phe Pro Ser Arg Ala Glu Met Glu Ser His Lys Arg Ala His Ala  
 515 520 525

Gly Pro Ala Ala Phe Lys Cys Pro Asp Cys Pro Phe Ser Ala Arg Gln  
 530 535 540

Trp Pro Glu Val Arg Ala His Met Ala Gln His Ser Ser Leu Arg Pro  
 545 550 555 560

His Gln Cys Asn Gln Cys Ser Phe Ala Ser Lys Asn Lys Lys Asp Leu  
 565 570 575

Arg Arg His Met Leu Thr His Thr Asn Glu Lys Pro Phe Ser Cys His  
 580 585 590

Val Cys Gly Gln Arg Phe Asn Arg Asn Gly His Leu Lys Phe His Ile  
 595 600 605

Gln Arg Leu His Ser Ile Asp Gly Arg Lys Thr Gly Thr Ser Thr Ala  
 610 615 620

Arg Ala Pro Ala Gln Thr Ile Ile Leu Asn Ser Glu Glu Glu Thr Leu  
 625 630 635 640

Ala Thr Leu His Thr Ala Phe Gln Ser Asn His Gly Thr Leu Gly Thr  
 645 650 655

Glu Arg Leu Gln Gln Ala Leu Ser Gln Glu His Ile Ile Val Ala Gln  
 660 665 670

Glu Gln Thr Val Ala Asn Gln Glu Glu Ala Thr Tyr Ile Gln Glu Ile  
 675 680 685

Thr Ala Asp Gly Gln Thr Val Gln His Leu Val Thr Ser Asp Asn Gln  
 690 695 700

Val Gln Tyr Ile Ile Ser Gln Asp Gly Val Gln His Leu Leu Pro Gln  
 705                      710                      715                      720  
 Glu Tyr Val Val Val Pro Asp Gly His His Ile Gln Val Gln Glu Gly  
                          725                      730                      735  
 Gln Ile Thr His Ile Gln Tyr Glu Gln Gly Thr Pro Phe Leu Gln Glu  
                          , 740                      745                      750  
 Ser Gln Ile Gln Tyr Val Pro Val Ser Pro Ser Gln Gln Leu Val Thr  
                          755                      760                      765  
 Gln Ala Gln Leu Glu Ala Ala Ala His Ser Ala Val Thr Val Ala Asp  
                          770                      775                      780  
 Ala Ala Met Ala Gln Ala Gln Gly Leu Phe Gly Thr Glu Glu Ala Val  
 785                      790                      795                      800  
 Pro Glu His Ile Gln Gln Leu Gln His Gln Gly Ile Glu Tyr Asp Val  
                          805                      810                      815  
 Ile Thr Leu Ser Asp Asp  
                          820

<210> 9  
 <211> 5  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Peptide

<400> 9  
 Leu Val Asn Leu Leu  
   1                      5

<210> 10  
 <211> 5  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Peptide

<400> 10



Ala Val Asn Ala Ala

1 5

<210> 11

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Peptide

<400> 11

Leu Asp Leu Leu Leu

1 5

<210> 12

<211> 122

<212> PRT

<213> Human

<400> 12

Cys Asp Lys Cys Gly Lys Ser Phe Lys Lys Arg Tyr Thr Phe Lys Met

1 5 10 15

His Leu Leu Thr His Cys Glu Phe Val Cys Glu Asp Lys Lys Ala Leu

20 25 30

Leu Asn His Gln Leu Ser His Ala Thr Gln Thr Ala Leu Asp Leu Leu

35 40 45

Leu Asn Met Ser Ala Gln Arg Glu Leu Cys Lys Ile Cys Ala Glu Ala

50 55 60

Phe Pro Gly Arg Ala Glu Met Glu Ser His Lys Arg Ala His Cys His

65 70 75 80

Leu Cys Gly Gln Arg Phe Asn Arg Asn Gly His Leu Lys Phe His Ile

85 90 95

Gln Arg Leu His Leu Asn Ser Asp Asp Glu Thr Leu Ala Thr Leu His

100 105 110

Thr Ala Leu Gln Ser Ser His Gly Val Leu

115 120

<210> 13  
<211> 34  
<212> PRT  
<213> CHICK

<400> 13  
Asp Tyr Val Thr Leu Gln Asp Leu His Ser His Val Tyr Arg Glu Ser  
1 5 10 15  
Arg Asn Gly Glu Ser Gln Glu Ser His Gln Ile Met Glu Asp Gln Gly  
20 25 30

Gln Ala

<210> 14  
<211> 11  
<212> PRT  
<213> Rat

<400> 14  
Val Ser Ser Val Ile Glu Glu Glu Phe Asn Thr  
1 5 10